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ALIGNMENTS									
Result	LOCUS	DEFINITION	DEFINITION	DEFINITION	DEFINITION	DEFINITION	DEFINITION	DEFINITION	DEFINITION
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			NID						
			9456416						
			VERSION						
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			GI:156416						
			cell death protein; interleukin-1 beta converting enzyme.						
			L29052						
			Caenorhabditis elegans (strain N2) DNA.						
			9456416						
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			Caenorhabditis elegans						
			SOURCE						
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			Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidae;						
			Rhabdidae; Caenorhabditis.						
			1 (bases 1 to 7653)						
			Yuan,J., Shaham,S., Ledoux,S., Ellis,H.M. and Horvitz,H.						
			TITLE						
			The C. elegans cell death gene ced-3 encodes a protein similar to						
			mammalian interleukin-1 β -converting enzyme						
			Cell, 75, 641-652 (1993)						
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			Location/Qualifiers						
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 ACCESSION 281049
 NID 91627677
 VERSION 281049.1 GI:1627677
 KEYWORDS HRG.
 SOURCE Caenorhabditis elegans.
 ORGANISM Caenorhabditis elegans.
 Eukaryota; Metacida; Nematoda; Secernentea; Rhabditida; Rhabditidae;
 Rhabditina; Rhabditoidae; Paloderaiae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 3908)
 AUTHORS Burton, J.
 TITLE Direct Submission
 JOURNAL Submitted (21-Oct-1996) Louis, MO 63110, USA. E-mail:
 jes@scgier.ac.uk or rwmematode.wustl.edu

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 SOURCE ORGANISM Saccharomyces cerevisiae
 REFERENCE 1 (bases 1 to 38590)
 AUTHORS Sumrada,R.A. and Cooper,T.G.
 TITLE Nucleotide sequence of the *Saccharomyces cerevisiae* arginase gene (CARI) and its transcription under various physiological conditions
 JOURNAL J. Bacteriol. 160 (3), 1078-1087 (1984)
 MEDLINE 85054621
 REFERENCE 2 (bases 1 to 38590)
 AUTHORS Anderson,M.S., Muehlbacher,M., Street,I.P., Proffitt,J. and Poulter,C.D.
 TITLE Isopenetyl diposphate:dimethylallyl diphosphate isomerase. An improved purification of the enzyme and isolation of the gene from *Saccharomyces cerevisiae* CARI
 JOURNAL J. Biol. Chem. 264 (32), 19169-19175 (1989)
 MEDLINE 90037050
 REFERENCE 3 (bases 1 to 38590)
 AUTHORS Jamieson,D.J. and Beggs,J.D.
 TITLE A suppressor of yeast spn81/ded1 mutations encodes a very similar ATP-dependent RNA helicase
 JOURNAL Mol. Microbiol. 5 (4), 805-812 (1991)
 MEDLINE 91312117
 REFERENCE 4 (bases 1 to 38590)
 AUTHORS Zheng,Y., Cerione,R. and Bender,A.
 TITLE Control of the yeast bud-site exchange by cdc24 and stimulation of Grp42, Catalysis guanine nucleotide exchange by cdc24 and stimulation of Grp42.
 JOURNAL J. Biol. Chem. 269 (4), 2369-2372 (1994)
 MEDLINE 94131930
 REFERENCE 5 (bases 1 to 38590)
 AUTHORS Bussey,H., Storms,R.K., Ahmed,A., Albermann,K., Allen,E., Benes,V., Araujo,R., Abario,A., Barrell,B., Bruckner,M., Carpenter,J., Cherry,J.M., Chung,E., Churcher,C., Coster,F., Davis,K., Dusterhoff,R.W., Dietrich,F.S., Delius,H., DiPaolo,T., Dubois,E., Fritz,C., Goffeau,A., Hall,J., Heubel,J., Heublitz,H., Friesen,J.D., Hillier,L., Hunnicke-Smith,S., Hyman,R., Johnston,M., Kalman,S., Kleine,K., Komp,C., Kurdi,O., Lashkarji,D., Lew,H., Lin,A., Lin,D., Louis,E.J., Marathe,R., Messenguy,F., Newes,W., Mirtiatti,S., Moestl,D., Muller,Auer,S., Namath,A., Neutzwisch,U., Oeffner,P., Pearson,D., Peter,F.X., Pohl,T.M., Purnell,D., Schafer,M., Scharfe,M., Scheeres,B., Schramm,S., Schroeder,M., Tettelin,H., Urrestarazu,L.A., Ushinsky,S., Vierendeels,F., Visser,S., Voss,H., Walsh,S.V., Wambutt,R., Wang,Y., Wedler,E., Wedler,H., Winnert,E., Zilch,W.W., Zoller,A., Vo,D.H. and Hani,J.
 TITLE The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI
 JOURNAL Nature 387 (6632 Suppl), 103-105 (1997)
 MEDLINE 97313271
 REFERENCE 6 (bases 1 to 38590)
 AUTHORS Schiltenstedt,G. and Silver,P.A.
 TITLE Unpublished
 REFERENCE 7 (bases 1 to 38590)
 AUTHORS Hall,J., Ahmed,A., Bussey,H., Wang,Y. and Wimmet,E.
 TITLE The sequence of *Saccharomyces cerevisiae* chromosome XVI left arm
 JOURNAL Unpublished
 REFERENCE 8 (bases 1 to 38590)
 AUTHORS Weber,L. and Byers,B.E.
 TITLE me5, a novel meiotic mutation
 JOURNAL Unpublished (1992)
 REFERENCE 9 (bases 1 to 38590)
 AUTHORS Bussey,H.
 TITLE Direct Submission
 JOURNAL Sub205 Dr. Field Ave., Howard Bussey, McGill University, Biology, 1205 Dr. Field Ave., Montreal, Quebec H3A 1B1, Canada
 REFERENCE 10 (bases 1 to 38590)
 AUTHORS Jia,Y. and Cherry,J.M.
 TITLE Direct Submission

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RESULT 2
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 VERSION 781049.1 GI:1627677
 KEYWORDS HTG.
 SOURCE Caenorhabditis elegans.
 ORGANISM Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;
 Caenorhabditis elegans.
 AUTHORS Rhabditina; Rhabditoidae; Rhabditidae; Peioderinae; Caenorhabditis.
 REFERENCE 1 (bases 1 to 39908)
 AUTHORS Burton, J.
 TITLE Direct Submission
 JOURNAL Submitted (21-OCT-1996) Louis, MO 63110, USA. E-mail:
 jesesanger.ac.uk or rwenemateode.wustl.edu

REFERENCE	AUTHORS	JOURNAL	MEDLINE	DOCUMENT	TITLE	FEATURES	source	Query Match	Best Local	Similarity	Score	Length							
2 (bases 1 to 39908)	Wilson,R., Binscough,R., Anderson,K., Baynes,C., Berks,M., Coulson,J., Burton,J., Connell,M., Copsey,T., Cooper,J., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A., Fulton,L., Gardner,A., Green,P., Hawkin,T., Hillier,L., Jier,M., Johnson,L., Jones,M., Kershaw,J., Kirstein,J., Laister,N., Latrell,P., Lightning,J., Lloyd,C., McMurrary,A., Mortimore,B., O'Callaghan,M., Parsons,J., Percy,C., Rifkin,L., Roopra,A., Saunders,D., Showman,R., Smaill,N., Smith,A., Sonnhammer,E., Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaughn,K., Waterston,R., Watson,A., Weinstock,L., Wilkinson-Sprout,J. and Woldman,P.	Science	9415018	Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information. For a graphical representation of this sequence and its analysis see: http://webace.sanger.ac.uk/cgi-bin/display/db-wormacc&class=Sequence&object=C4BD1	2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans	/gene="C4BD1_2" /note="similar to Caspase recruitment domain, ICE-like protease (caspase) P20 domain, ICE-like protease (caspase) p10 domain.; cDNA EST EMBL:D1553 comes from this gene; cDNA EST Yk198f10_5 comes from this gene; cDNA EST Yk491a5_5 comes from this gene"													
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						/codon_start=1 /protein_id="CAB02846_1" /db_xref="PID:@134741" /db_xref="PID:93875048" /db_xref="SPREMBL:002227" /translation="MTKPLHDIAQCQKIAEFVQNSYDNEFELDSKSSNNVSYLMNRDKFNLNKTTHKLNKTYKVTLPOTIDENTARQKLSKWSWCFRKETRIVDQHPLTLELUNNEPFRKQHPLKQWTAKGMLPLSLUMLNDVHINEKURVLDVSYQTFENLHERNNVQYQTFECKMELPELREMDCTSLSLSDCILECLKTQLSPPNTISVTEATSQYNDVQYQTFECKMELPELREMDCTSLSLSDCILECLKTQSENQNQNTISPKLTQYRSMQFDSISVQNGKCLTGFMSNQLCSNGTLLVEKARPTBASSLCGCCIRHNMDESKLSLKDEISKTAMSFLLENRVSIMTEKESSKACHNMQGIISISSLSCMEKVESNDITTCLELLTNSSALNDSLQELYSSNVDKIGQONAYSTEK" /gene="C4BD1_2" /complement(join(6258..6349,6876..10501,10501..10780, 7612..7815,8128..9055,10248..11120))													
						gene		Query Match	95.0%	Score	950;	DB	21;	Length	39908;				
						CDS		Best Local	98.6%	Pred. No.	0..00e+00;	Matches	9;	Indels	5;	Gaps	4;		

